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Guidelines for Authors

Articles, species profiles, reviews, research updates, personal perspectives, news items and announcements for the noticeboard are invited on topics relevant to the newsletter's focus.

Material for edition number 18 should be sent to Dr PJ Stephenson (StephensonPJ@gmail.com). Articles should be under 3,000 words and follow the format of this edition. Reference citations should be in APA format. The editor reserves the right to edit all contributions for style and content.

Message from the Chair

Andrew Taylor

Chair, IUCN SSC Afrotheria Specialist Group

Dear Afrotheria Specialist Group colleagues,

I hope you are all well and have managed to keep your heads above water during the last year. Hopefully you have been able to return to some semblance of normalcy over the last few months although, if your experience has been anything like mine, your ability to travel remains limited, and this will no doubt have impacted your work.

Although we are now into the next IUCN quadrennium, things have been slow to get going and we have not yet re-assembled the group members. Technically, all who were members during the last four years are still members, and the changeover is expected to start during October/November. So, I (or the section coordinators) will be getting in contact with you soon to follow up. This is an opportunity to bring in new members if you know of biologists and conservationists working on our taxa that you think will make a genuine contribution to the group.

As I mentioned last year, I anticipate us starting a process to reassess the conservation status of all our species during the next quadrennium, so please be ready to assist if you are able. This can be a slightly protracted process, especially for the section coordinators, but it is necessary for the ongoing conservation support of our species.

As always, the newsletter remains one of the few ways we have to keep our group relevant under the current difficult funding climate. It is one of the targets we set ourselves that is manageable without financial resources and helps us stay on the radar of the IUCN SSC. Please keep supporting the newsletter by submitting articles to

the next edition in 2022. Thanks again to PJ Stephenson for continuing as the newsletter editor and to those who submitted articles.

I wish you well for the coming year.
Andrew

Andrew Taylor, Gauteng, South Africa
1 December 2021

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Articles

Anthropogenic pressures on the aardvark (*Orycteropus afer*) in Monts Kouffé Protected Forest in Benin

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Introduction

Since the beginning of the twentieth century, increased demand for natural resources from a growing human population has exerted enormous pressures on west African ecosystems (Sinsin & Kampmann, 2010). Located in the Dahomey gap, Benin has ecosystems of international importance serving as refuge for west African fauna and flora (MCVDD, 2017). The creation of protected areas was supposed to counter the advance of agriculture and other forms of pressure on natural ecosystems, but today these pressures strongly affect protected areas (Zakari et al., 2018). Since the end of the 1980s, some protected forests in Benin (e.g., Lama, Toui-Kilibo, Ouémé Supérieur, Bassila, Goungoun, Sota, Wari Maro, Monts Kouffé, Agoua, Penessoulou) have benefited from participatory management plans but the impact of sustainable conservation on these massifs is not tangible (Assogbadjo & Sinsin, 2010). The Monts Kouffé Protected Forest, although it is classified and benefiting from a participatory development plan, is under strong human pressure. Mammalian fauna is not spared from this anthropogenic pressure (Dotché, 2016).



Figure 1. Aardvark in the Pendjari Biosphere Reserve. Camera trap photo courtesy of the NGO “Organisation pour la promotion de l’éducation des filles au Bénin” (OeBENIN).

The aardvark (*Orycteropus afer*; Fig. 1) is currently confined to protected areas in Benin, in particular the central and northern areas. Although it is rarely observed during wildlife counts, signs of its presence (such as footprints and burrows) confirm its occurrence in the Monts Kouffé Protected Forest (MKPF) and in national parks (Pendjari and W biosphere reserves) (Akpona & Daouda, 2011). Aardvarks are sought after by witch

doctors and traditional healers. They are also preyed upon by large carnivores such as hyenas or leopards. Although no studies have focused on the species to identify hunting pressure, the species deserves special attention (Akpona & Daouda, 2011). The aim of this study was therefore to assess the impact of anthropogenic pressures on the survival of aardvark in MKPF.

Methods

Study Area

The Monts Kouffé region in Benin is located between the departments of Borgou, Donga and Collines. It is framed by meridians 1°30' and 2°30' East longitude and parallels 8°30'–9°15' North latitude. The Monts Kouffé forest complex, with an area of 180,300 ha, is located in central Benin, straddling the municipalities of Bantè, Bassila, Ouessè and Glazoué (Akouehou 2004). It is bounded to the North by the classified forest of Wari-Marou, to the South by the Municipality of Bantè, to the East by the Municipality of Ouessè and to the West by the Municipality of Bassila (Odjoubere et al. 2013).

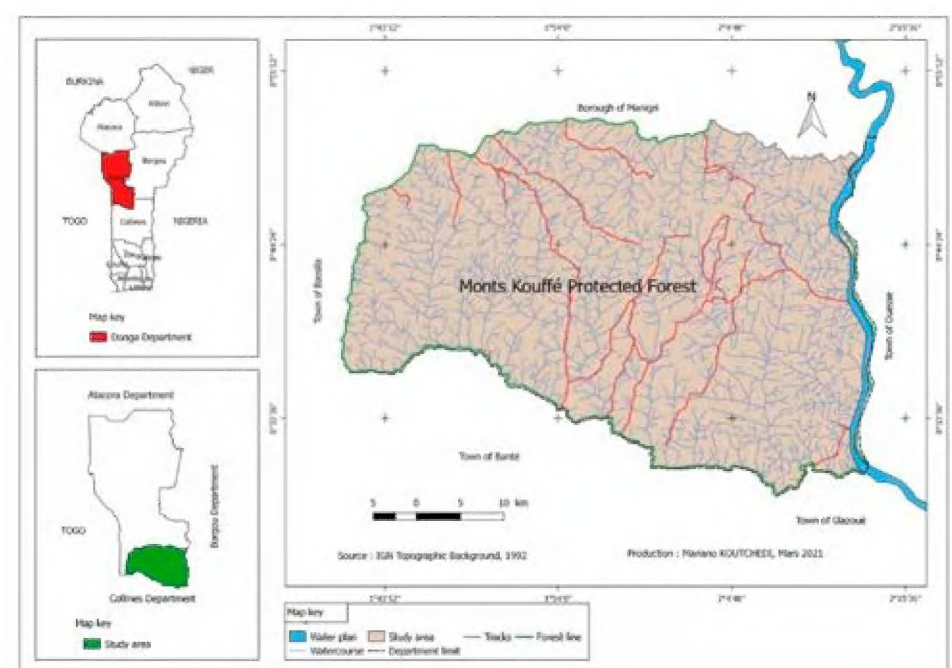


Figure 2. Geographical location of the study area.

The Monts Kouffé region is influenced by the humid Sudanese tropical climate characterized by two seasons: a marked dry season which lasts five months (November to March) and a rainy season which lasts from April to October. The average annual rainfall is 1200 mm and the average annual temperatures are 26 or 27°C (Houinato & Sinsin, 2001). The dominant geological substratum in the region consists of very old crystalline formations of the “Dahomeen” type. The bedrock is granito-gneissic in nature and displays residual knolls (inselbergs), two of which represent the Monts Kouffé where the classified forest is located. The altitude of the larger inselberg is 523 m above sea level, and 342 m for the smaller one (Toko, 2005). The types of plant formations characterizing the study area are: open forests, dense dry forests with *Anogeissus leiocarpus*, gallery forests with *Pterocarpus santalinoides*, wooded savannas with *Isobertlinia doka*, *Pterocarpus erinaceus*, *Isobertlinia tomentosa*, tree and shrub savannas presenting a dense shrub layer with a tree layer dominated by *Burkea africana*, *Detarium microcarpum*, *Terminalia avicennioides*, fallows characterized by species such as: *Strychnos spynosa*, *Nauclea latifolia* in their young age (Tchabi et al., 2012).



Figure 3.Vegetation cover in MKPF: gallery forest (top); dense dry forest (bottom). Photos: M. Koutchédi.

Data collection

Our data combines observations in the natural environment with information collected through a population survey. The study was carried out between November and December 2020

Since the aardvark is a nocturnal, burrowing and shy species, direct observations were very difficult during the day. Nonetheless, daytime reconnaissance walks with field guides allowed collecting useful information on the species, like indirect trace of activities as well as indices of human activities in the study area. This method consisted of walking paths of least resistance (such as animal tracks, human tracks, clear undergrowth, ridges). Two observers walked in front of the tracker and the person who noted down all observations, thus determining several variables (sign, species, age, class, presence of burrows). Observations were converted into Kilometric Abundance Index (KAI), which is “a common measure used in wildlife studies because it allows a straightforward comparison of species abundance in different sites or at different times” (Preatoni et al., 2012).

The identification of the main forms of anthropogenic pressure on the aardvark population in the study area is based on information obtained through interviews of local population. A sample of the population (100 people) was drawn up by the reasoned choice method, which made it possible to identify hunters, farmers, animal remains sellers, foresters, village chiefs, in five villages bordering the forest. Questions were also asked to the respondents to understand the origin of the trophies of the species observed during the surveys.

Respondents chosen were at least 30 years old to be sure of the veracity of the information provided by the interviewee and to obtain information on local perceptions of the past and current abundance of the

species. They were also a resident of the study area so as to provide information of relevance. The one hundred respondents included 66 farmers, 25 hunters, 7 housewives, and 2 sellers of animal remains; seven were women, 93 were men. This gender bias reflects the fact that very few women were found to have any knowledge of the target species.

Table 1. Survey walks in the hunting areas of the Monts Kouffé Protected Forest.

Hunting area	Area (ha)	No. days	Distance (km)
Okouta-ossé	10,861	2	14.7
Banon-Akpassi-Bante	36,258	5	30.4

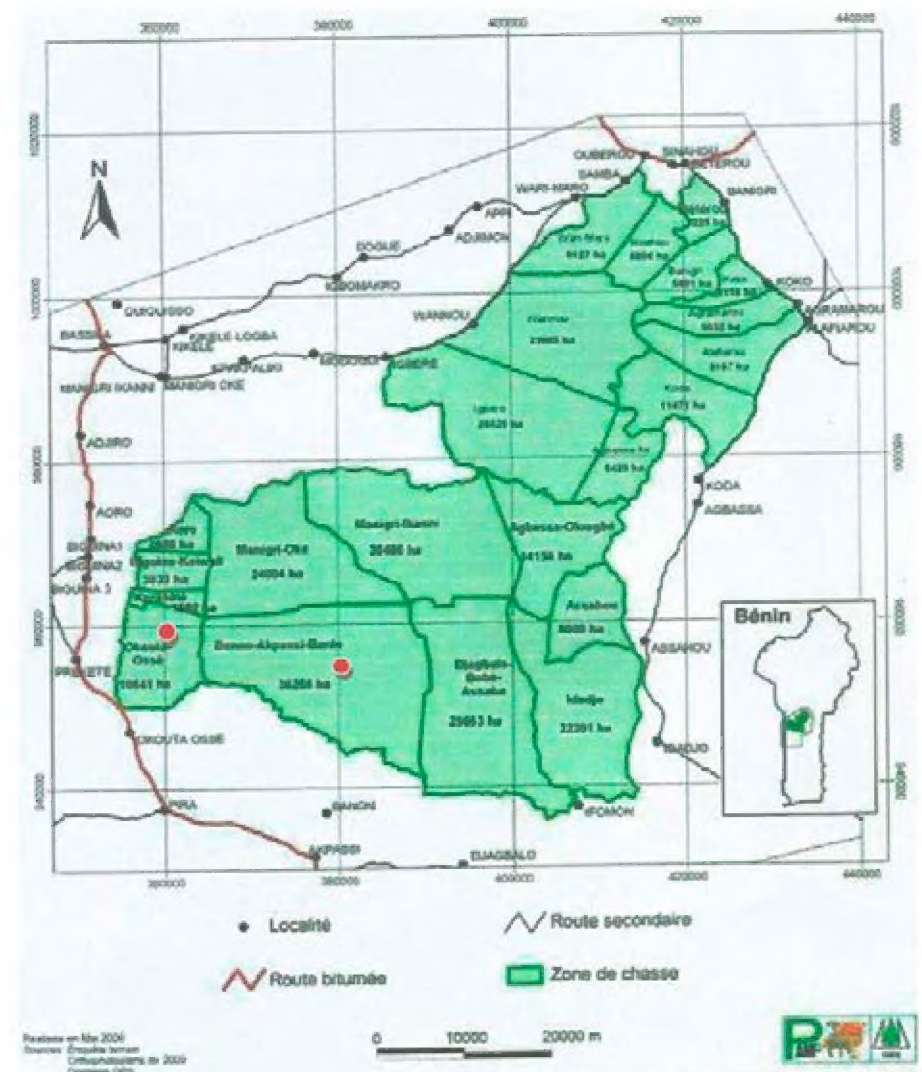


Figure 4. Map of MKPF hunting areas. The red points indicate the hunting areas covered. Map produced during PAMF (Projet d’Amenagement des Massifs Forestiers) project in 2006.

Data analyses

The responses to the questionnaires were coded and processed using Excel (Microsoft Corporation, 2013). Parameters calculated were:

- Relative frequency (Fr) of citation of the perceived causes of decline of aardvarks according to the people interviewed. n: number of people who cited a given cause and N is the total number of people interviewed.
- Frequency of past and current perceived abundance of aardvark according to the people surveyed. n: number of people who cited a given abundance category for the species and N is the total number of people interviewed.
- Kilometre Abundance Index. n: Number of observations for aardvark burrows and D: Total distance travelled.

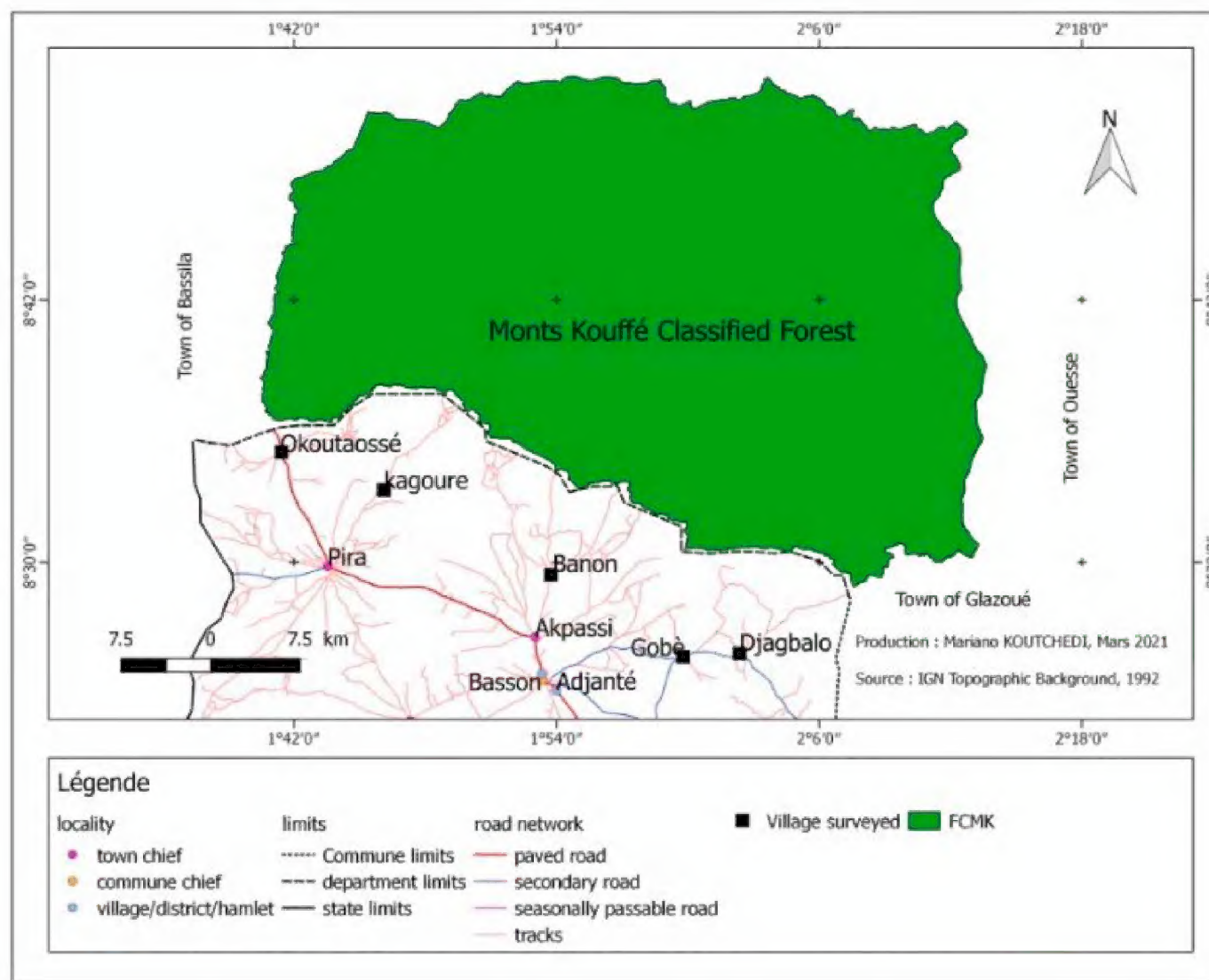


Figure 5. Map showing survey villages.

Table 2. Probable threats to the aardvark according to survey respondents.

Village	Number of respondents citing the pressure				Number of people surveyed
	Poaching	Transhumance	Logging	Others	
Akoutaossé	7	7	4	2	20
Kagourè	12	5	1	2	20
Banon	20	0	0	0	20
Bobè	14	5	1	0	20
Djagbalo	16	1	2	1	20
Total (%)	69 %	18 %	8 %	5 %	

Results

Pressures identified by respondents

All respondents considered the aardvark as an endangered animal, due to the strong direct and indirect anthropogenic pressures on the animal and its habitat. Causes listed were poaching, transhumance, logging and a variety of other reasons (including low rate of reproduction preventing population recovery).

Poaching was considered by 69 per cent of respondents to be the main possible reason for aardvark population decline in the MKPF, followed by transhumance (18%; the movement of livestock from one grazing ground to another in a seasonal cycle) and logging (8%).

Poaching was mentioned in all the villages surveyed. Statements made about the quality of the species' meat and the alleged prowess of these organs and bones in traditional medicine attest to the interest of local population in aardvark as a source of bushmeat, charms and curios. Such appeal might explain why some hunters are ready to spend a lot of time hunting aardvarks. The locals believe that the species was poached in the MKPF to such an extent that it is hardly seen nowadays. This is probably compounded by the fact that young and adult aardvarks seem to be poached indiscriminately in all the villages surrounding MKPF. During our survey all of the species parts observed are considered obtained after poaching of the species (Figure 6).

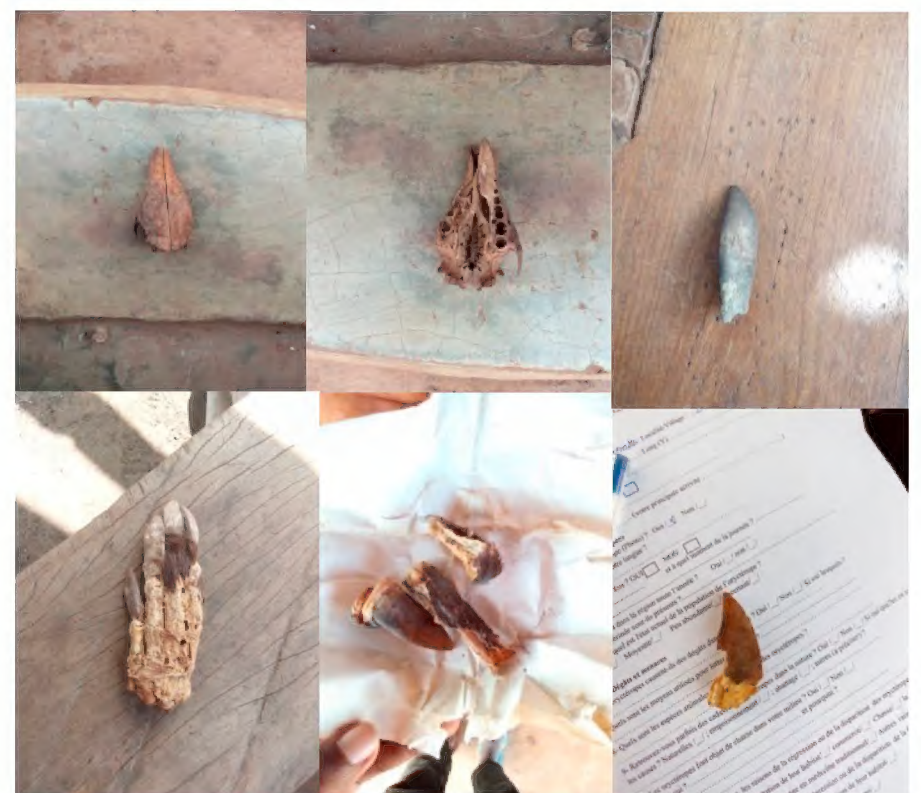


Figure 6. *Orycteropus afer* trophies observed during surveys, including skulls, paws, nails and bones. Photos: M. Koutchédi.

All respondents claimed that there has been a strong decline in aardvarks in MKPF compared to twenty years ago, when the species was said to be abundant. In particular, 55 % of those surveyed said that the aardvark is currently very rare in MKPF compared to 39 % who said the species is extinct. Only 6 % of respondents gave a mixed (uncertain) response about the abundance of the

species (Table 3). Interviewees said that to see an armadillo nowadays, one must venture far into the forest and spend several days there. Most of those interviewed admitted to having last seen an armadillo over 15 years ago.

Table 3. Perception of respondents on the current state of *Orycteropus afer* populations

Village	Very rare	Extinct	Un-certain	No. people surveyed
Akoutaossé	5	13	2	20
Kagourè	6	13	1	20
Banon	10	8	1	20
Bobè	18	2	0	20
Djagbalo	16	3	1	20
Total	55 %	39 %	6 %	

Field observations

Investigations in the natural environment have shown that the Banon-Akpassi-Bante hunting area is the most abundant in terms of the armadillo burrows in MKPF, with 76.5% of observations and a Kilometric Abundance Index (KAI) of 0.42, compared with 23.5% of observations (KAI 0.27) for the Okouta-ossé hunting area. It should be noted that only 17.6% of the burrows observed were active against 82.4% abandoned and all the active burrows were observed in the Banon-Akpassi-Bante hunting area. This could be explained by the fact that the armadillo may no longer exist in the Okouta-ossé hunting area. The Kilometric Abundance Index of burrows for two hunting area is (KAI= 0.37).

Table 4. Burrows identified in field surveys. KAI = Kilometric Abundance Index.

Hunting area	No. armadillo burrows	Km walked	KAI
Okouta-ossé	13	14.7	0.27
Banon-Akpassi-Bante	4	30.4	0.42



Figure 7. Different types of armadillo burrows observed in MKPF (left to right). old closed burrow; old half-closed burrow; active burrow. Photos: Koutchédi & Koami.

Discussion

This study found that poaching is the most important threat to armadillos in MKPF. The large proportion of abandoned burrows found in the field survey, and the local perception that the species is very rare, confirm the

impacts of this pressure on the species. This finding agrees with the IUCN (2015) assessment that identifies habitat loss due to agriculture and hunting as potential threats. A study by Dotché (2016) identified seven pressures on the mammalian fauna of the MKPF, namely honey extraction, logging, overgrazing, wildfires, poaching, charring and noise pollution from chainsaws and trucks which was leading to the gradual disappearance of mammals from the MKPF.

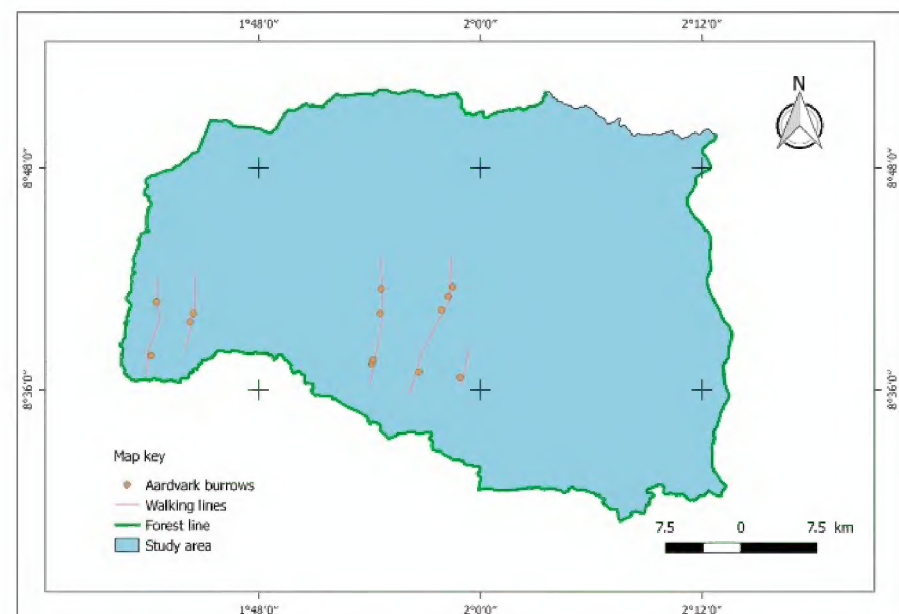


Figure 8. Map showing the distribution of burrows.

Studies on armadillos in the Kalahari in South Africa indicated that the survival of armadillos can be threatened by climate change related droughts, which likely caused a decline in their prey resources (Rey et al., 2017; Weyer et al. 2020). However, IUCN (2015) noted that the impacts of threats to the armadillo and its current demographic trends are not known and no targeted conservation measures are recommended at present.

The results of this study do not bode well for the future of the armadillo in Monts Kouffé Protected Forest. Without conservation action, we will likely see the local extinction of this keystone species. It is therefore necessary to secure funds as soon as possible for a detailed study on the size of the armadillo population in MKPF. In addition, the authorities in charge of the MKPF need to initiate a long-term ecological monitoring programme, as well as develop and implement with relevant NGOs an action plan for the conservation of populations bordering the forest. Only with such urgent action can be hope to secure a future for the armadillo in this important forest in Benin.

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Social status and social network in a captive rock hyrax (*Procapra capensis*) group

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Introduction

The rock hyrax (*Procapra capensis*) has been studied mostly in the wild (Barocas et al., 2011; Demartsev et al., 2016; Demartsev et al., 2019; Hoeck, 1989; Koren & Geffen, 2008), and to a lesser degree in captivity (Fourie, 1976; Koresh et al., 2016). Hyrax social network and hierarchy has been examined in relation to longevity and quality of life (Barocas et al., 2011), physical characteristics (Koren & Geffen, 2008) and vocal abilities (Demartsev et al., 2016) in their natural habitat. However, their social status in captivity has not been studied.

In the spring of 2019, we studied a group of captive rock hyraxes to understand their social composition in captivity. The group has been in an enclosure located on campus for a few years (Koresh et al., 2016), but their social interactions had not been observed. One of the study's goals was to find out whether hyrax behaviours in captivity are similar to behaviour in the wild where mothers are dominant over juvenile females and bachelor males (Koren et al., 2006; Koren & Geffen, 2008).

Sites and Methods

A group of 18 captive rock hyraxes was observed over 15 days between April 14th and May 20th, 2019. The enclosure was located in Bar Ilan University, Ramat-Gan, Israel (location: 32.066, 34.839). The size of the enclosure was 5.42×5.55×2.24 metres. It includes a big rockery in the middle including lairs for hiding. A small plywood shed was placed close to a concrete platform allowing food to remain fresh for longer. Two doors locked the enclosure and the observer sat in the middle area. As both the ceiling was covered with a net and the ground was paved with concrete, the enclosure was completely sealed. Food was given once a day and included mostly cabbage supplemented with bell peppers, Carob (*Ceratonia siliqua*) leaves and pods, Greek strawberry tree (*Arbutus andrachne*) leaves and fruits and occasionally Nerium (*Nerium oleander*) leaves.

The group included three adult females that were born and captured in northern Israel (Ein Ya'akov 33.007, 35.231) and 15 captive-born juveniles (14 months old at the time; five females and ten males). The group member list is noted in Table 1. The enclosure is shown in Figure 1.

Following Altman (Altman, 1974), all occurrences were documented. Observations of individuals that could not be identified, or observations where the beginning or ending time was unclear, were excluded from the data set. Since rock hyraxes have a poor ability to thermoregulate, the starting time was also affected by ambient temperature. All interactions were represented as dyads (i.e., between

two individuals), and up to five individuals interacting were scored in the final data. When more individuals were involved in an interaction, it was considered a mass brawl or a huddle, depending on the context. Both the social network and the agonistic behaviours were documented as directed, containing an active individual and a passive individual that received the gesture.

An association index used in past studies (Bar Ziv et al., 2016), which normalizes each participant's observational time (the ratio of each individual's observed time by the observation's duration), was used in an altered version for this study. Both social interactions and agonistic interactions were calculated as a relative duration (i.e., the ratio of the interaction duration by the total current observation duration in minutes). The hierarchical rank was calculated considering the agonistic interactions according to David's score (DS; David, 1987) and De Vries' normalization of DS (NormDS; De Vries et al., 2006). DS was developed to rate Chess players' competence according to their winnings in addition to the rivals' winning and losing rates. It shows an individual's hierarchical rank in relation to rivals it did not necessarily meet. Since it assumes that there are enough interactions to decide each individual's rate (i.e., a big enough sample size and no observational insufficiency), and that the individuals have similar winning potential, NormDS was created to see differences in groups that do not fit one or more of those assumptions.



Figure 1. The enclosure from the observer's point of view. Yellow arrows show location of CCTV cameras.

Results

In total, the animals were observed for 4,102 minutes. 2,474 minutes of which were in the morning (i.e., starting from 6:55 am and ending until 12:35pm) and 1,628 minutes at afternoon (i.e., starting from 11 am and ending until 6pm). Although composing less than 1% of the observations' duration (27.55/4,105 min), feeding included about 12% of all agonistic interactions (i.e., 230.15 min) and 11% of the social interactions (i.e., 446.5 min).

Table 1 show the results for the D's calculation based on 376 agonistic observations. The three oldest females, Chumsha, Malka and Maria (i.e., DS rank 1 to 3) were the most dominant individuals. When considering the agonistic interactions, about 41.6% (156/375) of them involved at least one of senior females. When looking at the social interactions, about 55.6% of them (470/845) included either one of the senior females.

Table 1. Individual names and social ranks, based on David's score (DS; David 1987). W/C specifies whether the animal was wild-born or captive-born. DS shows the unnormalized David's score and Norm DS shows it De Vries' normalized DS.

Rank	Name	Sex	W/C	Ds	Norm Ds
1	Chumsha	F	W	12.17	9.1761
2	Malka	F	W	11.1	9.1166
3	Maria	F	W	6.93	8.8850
4	Shimi	M	C	2.55	8.6416
5	Maker	M	C	2.47	8.6372
6	Trouble	M	C	1.7	8.5944
7	Eran	M	C	1.67	8.5927
8	Beni	M	C	0.38	8.5211
9	Libi	F	C	0.16	8.5088
10	Meshi	M	C	-1.3	8.4277
11	Sela	F	C	-1.67	8.4072
12	Raphi	M	C	-3.24	8.3200
13	Doctor	M	C	-3.27	8.3183
14	Cochava	F	C	-3.83	8.2872
15	Shlush	M	C	-4.56	8.2466
16	Hedva	F	C	-6.93	8.1150
17	Nikita	M	C	-9.43	7.9761
18	Tura	F	C	-37.97	6.3905

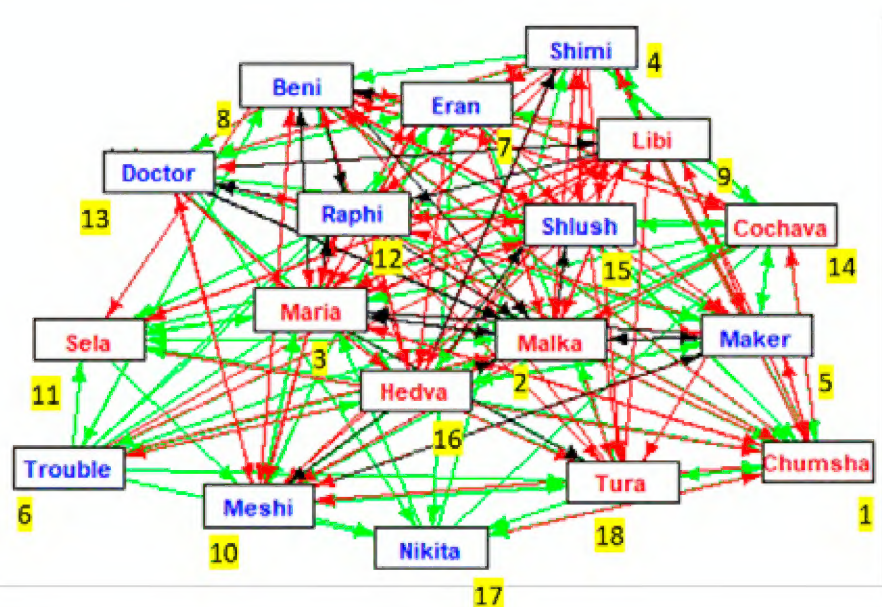


Figure 2. A summary of the social network. The number under each name represent the individual's social rank based on Ds. The arrow shows the recipient side of the interaction and each dyad is the summary of the relative interaction. Green links show a weak connection (i.e., less than 5% of the observations' time), red shows a medium strength relationship (i.e., 5-19% of the time) and black represents a strong and long lasting connection between the two hyraxes (i.e., more than 20% of the observation time spent together).

Figure 2 show the social network based on 845 observations. The network's density is approximately 0.83 (255/306 connections), which is much higher than expected considering hyraxes in the wild spend most waking hours browsing in solitude. It may be due to forced

association in the captive setting. Another reason might be stress. Ten out of 23 strong (in black) connections included a female, Malka, either as the recipient or an initiator of a social behaviour. It may suggest a central location in the group – both for social and agonistic interactions.

Although having an extremely low D.S when unnormalized, the lower-ranked individuals (e.g., Nikita and Tura) seem to have a much different situation when looking at the normalized score. This might be due to an extremely low observations rate for those individuals – as Nikita participated in only 17 interactions and Tura in only 29 (while mostly being on the passive side).

The social network (Fig. 2) shows that, though being mostly a recipient of an interaction, Malka also initiated four strong connections in which she was the initiator. Malka's (Ds 2 in rank) centrality in the group seems to correlate with mutual social interactions or vice versa. As in general, many connections seem mutual to some extent - as Malka does not only receive many favours from others, but also initiates many relationships.

Discussion

Although hyrax groups are not steeply hierarchical, senior females tend to have higher social status and be more aggressive (Barocas et al., 2011; Koren et al., 2006). In accordance with past studies, the current study found that, even in captivity, females held the highest social and hierarchical ranks. When examining social interactions in this study, the most frequent interactions were male-female dyads (i.e., an initiating male and a recipient female) including 235 out of 845 cases. Since the recipient part is the "favour receiver", it may suggest higher female social status in this case. On the other hand, when considering only the agonistic interactions, male – male dyads were the most common. This may be due to the fact observations were made in the pre-mating season period which is characterized by high levels of intersexual and intrasexual tension and competitiveness (Demartsev et al., 2019; Ilany et al., 2011). On the other hand, since 10 out of 18 individuals in the enclosure were males it could be only due to being the majority in the population.

The results show that the social and hierarchical structure of this captive hyrax group has similarities and differences to that found in the wild. Similar to wild animals, older females and especially mothers were dominant over other group members, and seem to have the highest hierarchal rank in addition to a very central social rank. Perhaps, since the original female founders were part of the same social group in the wild, and the juveniles were either related or grew up together since birth, the group was strongly cohesive. This cohesiveness is reflected by the high graph density and high rate of mutual relationships. Alternatively, this apparent cohesiveness may be due to the animals' limited opportunities to keep their distance from each other in a captive environment.

One difference with the wild was that there was no clear resident male – one with a significantly higher social rank than other males. One reason might be that the observations were made while all males were still juveniles at a pre-dispersal age. They might be still seen by the adult females as pups and therefore there were no bachelor

groups. If that is the reason for high group cohesiveness it can be expected that, as the pups become adults, they might demonstrate a different social pattern. Another interesting observation was that, as opposed to what is seen at natural habitat, most of the songs were sung by the females.

In conclusion, we hope that this short study has contributed to the understanding of rock hyrax behavioural patterns and hierarchical structure in captivity. Although the rock hyrax is currently a species of low conservation concern (Butynski et al., 2015), a better knowledge of its social network in captivity can help planning hyrax cages in zoos and laboratories to ensure their welfare needs are met.

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Recommended fossil calibrators for time-scaled molecular phylogenies of Afrotheria

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Introduction

A phylogenetic framework provides the necessary evolutionary context for studies of comparative anatomy, life history, behaviour, biogeography, and systematics. Understanding taxonomy is also an essential pre-requisite for IUCN Red List assessments and the prioritisation of conservation action. Fortunately, molecular phylogenetic estimates have become increasingly common in the literature and often these trees are used as a basis for other studies. A standard phylogenetic analysis yields a tree whose branch lengths represent a measure of the genetic distance between included molecular sequences. However, time-scaled phylogenetic analyses require researchers to include calibration ages which are used to fit a model that transforms branch lengths into units of time. Often, an estimated temporal distance between taxa is of more interest than the genetic distance between DNA segments. The inclusion of *multiple* calibration ages (if they are available) is a best practice that brings all the available evidence to bear on the temporal model. While selecting the appropriate ages of calibrating fossil taxa is obviously important, perhaps more relevant is where those calibrations are applied in the tree. A misattributed fossil calibrator (e.g., using a stem-taxon to set a minimum age on a tipward crown-node) can severely distort the results.

Compared to some other continents, the fossil record of Africa through most of the Cenozoic is relatively limited. The set of known fossils that inform minimum diversification ages within and between the afrotherian orders can be sparse. For example, a hypothetical molecular study that examines the relationships among extant golden-moles will find that there are very few fossil chrysochlorid taxa; among these, the occurrences that might inform a minimum age for the crown-clade are mostly immaterial because the fossils themselves are quite recent (only a few million years old) and the DNA alone already suggests that relevant golden-mole diversifications are older than the candidate calibrators. Only slightly better, a molecular study of extant sengis will identify a single fossil that provides a minimum age for the Rhynchocyoninae-Macroscelidinae split, but no other fossils that can be securely attributed (e.g., same genus as extant sengis) that are also old enough to be of value for estimating diversification ages within the order. It is a conundrum. In such cases, we recommend the inclusion

of multiple afrothere outgroup taxa in the molecular data set so that several fossil taxa can be applied as *external* age calibrations.

Our aim is to provide a summary of fossil calibrators that can be used in molecular phylogenetic assessments of Afrotheria. The literature that documents these fossils, and discusses their ages and affiliations, is somewhat scattered. Included in this contribution are the oldest extinct species that are (in our opinion) securely attributable to stem lineages. Each informs a minimum age for the adjacent rootward tree node. We then assemble a large DNA super matrix that includes 32 genes and 39 afrotherian genera – including recently extinct elephants and sea-cows. A time-scaled phylogenetic estimate is derived from this data set with explicit inclusion of fossil taxa in the analysis.

Methods

The DNA data set used here compiled 32 gene segments (13 mitochondrial & 19 nuclear), all of which are amino-acid coding loci. Genes were aligned individually using the translation-guided alignment tool in Geneious v7.1.7 (Kearse et al., 2012). Alignments were concatenated into a 33,468 position supermatrix of which 11,070 are mitochondrial and 22,398 are nuclear. PartitionFinder v2.1.1 (Lanfear et al., 2016) was used to identify an optimal subsetting scheme. PF input data blocks were assigned as per gene and per codon position and we selected the greedy algorithm to search block combinations using GTR+I+G models. Subsetting schemes were assessed using the Bayesian Information Criterion and the best scheme recommended 17 partitions.

Bayesian phylogenetic analyses (standard & time-scaled) were performed with MrBayes v3.2.7 MPI (Ronquist et al., 2012) and supermatrix partitioning followed PF results. MCMC parameters were set to 2 runs, 16 chains, 16 attempted swaps per generation, 15M generations, and to sample in 1k generation increments. The first 5M generations were discarded as burnin yielding 10k post-burnin samples per run. Tree distributions were summarized using the MrBayes option for majority rule consensus plus all compatible groups. Convergence was assessed by the average standard deviation of split frequencies with a value <0.01 interpreted as sufficient run length.

For the time-scaled analysis, the ages of all extant taxa were fixed to zero and recently extinct taxa (3 elephants & 1 sea-cow) were fixed to the approximate ages of the source specimens for the genetic material. Calibrating fossil taxa were constrained to their respective stem lineages, fixed to the point estimate ages discussed above, and coded with all missing data. We applied an approximately flat clock rate prior and a 5M year SD for the unbounded truncated normal distribution on the root node. For the sample probability prior of the fossilized birth death model, we estimated that about 43% of extant afrotherian species were included in the molecular data set. Both standard and time-scaled analyses were constrained to root on the Paenungulata-Afroinsectiphilia split. GenBank accession numbers, sequences, alignments, and analysis input/output are available from the Dryad Digital Repository (<https://doi.org/10.5061/dryad.83bk3j9s2>).

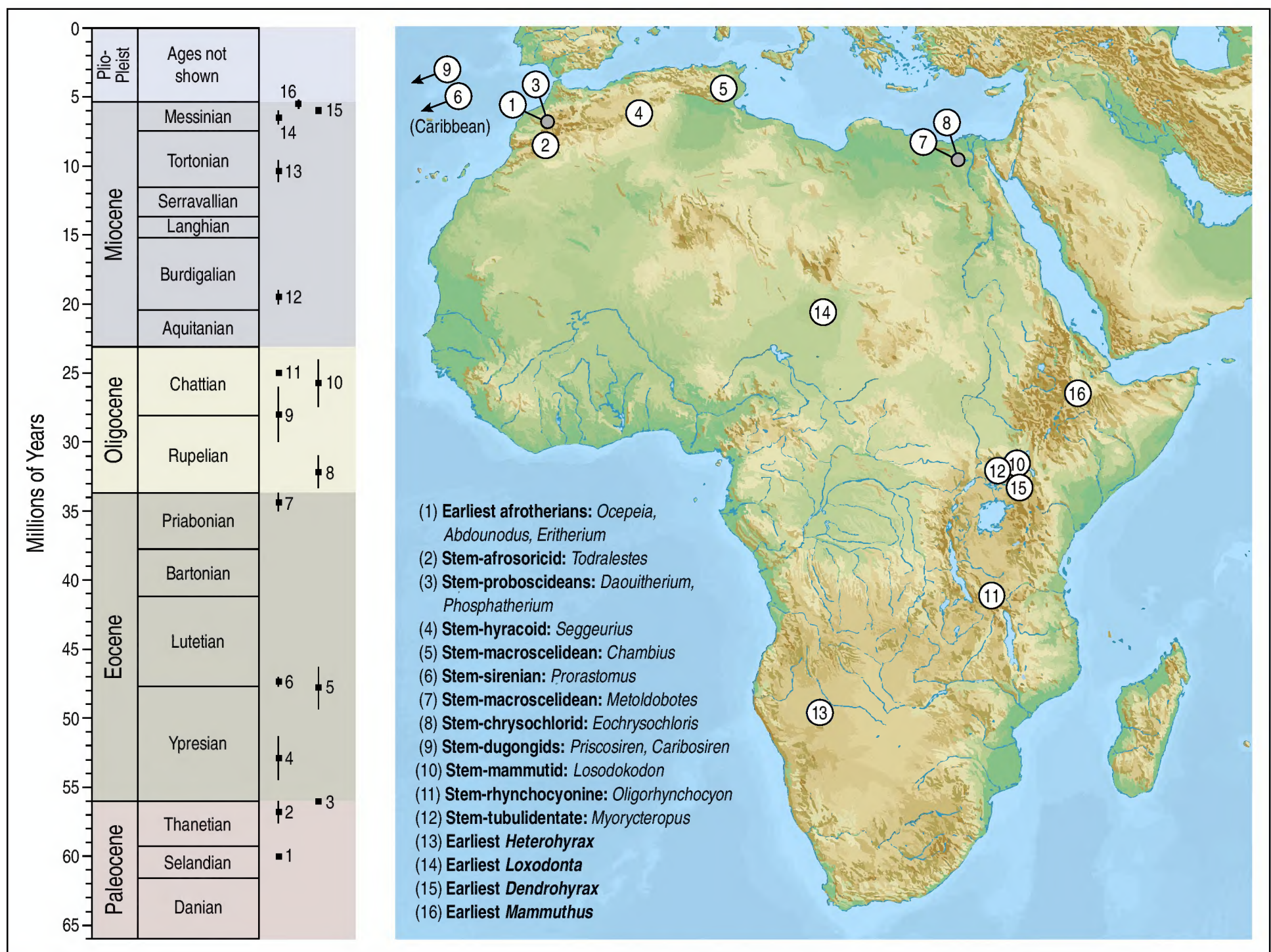


Figure 1. Geologic time-scale and mapped localities for fossil taxa discussed in the text. Open access base map is from Mapswire.com (CC-BY 4.0).

Fossil Calibrators

Stem-Hyracoidea. The earliest definitive stem-hyracoid is *Seggeurius amourensis* from the El Kohol Formation in Algeria (Court & Mahboubi, 1993). El Kohol is an Early Eocene (Ypresian) site with an estimated age range of 54.5–51.3 Ma (Seiffert, 2010a). For the purposes of phylogenetic calibration, 52.9 Ma should be a reasonable point estimate for this species. More fragmentary specimens of approximately the same age are known from the Ouled Abdoun Basin of Morocco (Gheerbrant et al., 2003; Kocsis et al., 2021).

Earliest-*Heterohyrax*. *Heterohyrax auricampensis* is the oldest known fossil species attributable to the genus *Heterohyrax* (Rasmussen et al., 1996). This taxon is known from Berk Aukas (Site I) in Namibia – an MN 9 fissure fill breccia. The locality's age is about 10.4 Ma (range 9.7–11.1 Ma., Tortonian, Late Miocene) (Rasmussen & Gutiérrez, 2010).

Earliest-*Dendrohyrax*. Known from the Aragai locality in the Lukeino Formation (Tugen Hills) of Kenya, *Dendrohyrax samueli* is currently the oldest fossil species attributable to the genus *Dendrohyrax* (Pickford & Hlusko, 2007). The age of the sandstone layer yielding this taxon is about 6 Ma (Messinian, latest-Late Miocene).

Stem-Proboscidea. The earliest putative stem-proboscidean is *Eritherium azzouzi* from Sidi

Chennane, bed IIa, in the Ouled Abdoun Basin of Morocco (Gheerbrant, 2009). However, some cladistic analyses have alternatively placed *Eritherium* as a basal paenungulate or tethythere (Cooper et al., 2014; Gheerbrant et al., 2018). Two additional fossil taxa, *Phosphatherium escuilliei* (Gheerbrant et al., 1996) and *Daouitherium rebouli* (Gheerbrant et al., 2002) are also from Sidi Chennane, but were recovered from the slightly younger Intercalary bed II/I phosphate level. While most workers consider *Phosphatherium* a stem-proboscidean, there's a possibility that it may instead be a basal tethythere (Cooper et al., 2014). Nevertheless, we consider *Daouitherium* to be an unquestionable stem-proboscidean (Cooper et al., 2014; Seiffert et al., 2012) and this fossil's antiquity is equivalent to *Phosphatherium*. The ages of the beds yielding these three taxa are tightly constrained at about 60 Ma (bed IIa, just below the Middle-Late Paleocene boundary) and 56 Ma (bed II/I, at the Paleocene-Eocene boundary) (Kocsis et al., 2014). For phylogenetic calibration, a conservative approach would be to consider *Daouitherium* (56 Ma) the oldest secure stem-proboscidean. However, some workers could convincingly argue that *Eritherium* (60 Ma) should take this title. Depending on the molecular data set, using any of these taxa to mark the minimum age for the origin of proboscideans may yield similar age estimates for most nodes in a phylogenetic tree.

Earliest-*Loxodonta*. The oldest fossils attributable to the genus *Loxodonta* are from the Toros-Menalla 266 site, in northern Chad (Sanders et al., 2010; Vignaud et al., 2002). The age of these specimens is about 6.5 Ma (range 6-7 Ma, Messinian, late-Late Miocene).

Stem-Mammutidae. Given that living proboscideans include only two genera, molecular phylogeneticists may elect to expand the diversity of sampled taxa within the order by including recently extinct elephants. Full mitochondrial genomes are currently available for mastodons (*Mammuth americanum*), woolly mammoths (*Mammuthus primigenius*), and straight-tusked elephants (*Palaeoloxodon antiquus*). Also, sequence read archives (SRA) of nuclear genomes are available for the latter two – *Mammuthus* has very good coverage and *Palaeoloxodon* is partial. If extinct elephants are included in a molecular analysis, a fossil calibrator for the family Mammutidae is appropriate. The earliest stem-mammutid is *Losodokodon losodoki* from the Eragaleit Beds at Lothidok, Kenya (Rasmussen & Gutiérrez, 2009). The temporal range of this site is 24-27.5 Ma (Chattian, Late Oligocene) (Boschetto et al., 1992) and a reasonable point estimate for the species is 25.8 Ma.

Earliest-*Mammuthus*. The earliest mammoth species is *Mammuthus subplanifrons* and the oldest specimens are from the Kuseralee member, Sagantole Formation of Middle Awash, Ethiopia (Sanders et al., 2010). The age of this site is about 5.5 Ma (range 5.2-5.8 Ma, Messinian, late-Late Miocene). If a molecular data set includes the extinct elephant *M. primigenius*, using *M. subplanifrons* to mark the minimum age of the genus is appropriate.

Stem-Sirenia. *Prorastomus sirenoides* is the earliest known stem-sirenian and was recovered from the Stettin Member of the Chapelton Formation in Jamaica (Savage et al., 1994). The limestone yielding this species is regarded as late-Early Eocene (terminal Ypresian) and is estimated at 47-47.8 Ma. A practical point estimate for this taxon is 47.4 Ma. For biogeographic context, it may be of interest that definitive stem-sirenians first appear in the African fossil record only shortly thereafter, about 45.5 Ma – starting with *Protosiren fraasi* from the Lower Building Stone member of the Mokattam Formation in Egypt (Zalmout & Gingerich, 2012). Further, a petrosal specimen from Chambi, Tunisia (Benoit et al., 2013), that might represent the oldest record of Sirenia from Africa, is approximately contemporaneous with *Prorastomus* from Jamaica.

Stem-Dugongidae. Steller's Sea-Cow, *Hydrodamalis gigas*, is a recently extinct sirenian that is well-represented with full nuclear and mitochondrial genomes. With only two extant sirenian genera, molecular phylogeneticists may elect to expand the order's taxon sample by including *Hydrodamalis* in their data sets. Among living sea-cows, this species is unequivocally placed as sister to *Dugong* and is therefore a dugongid. Phylogenetic estimates for the earliest known stem-dugongid vary slightly between studies. Using the largest and most current morphological character matrix of living and fossil sirenians, parsimony methods (Velez-Juarbe & Wood, 2018) and our Bayesian assessment of the same data both agree that *Priscosiren atlantica* and *Caribosiren turneri* are early taxa affiliated with the Dugongidae stem. Both species are known from the San Sebastian Formation in Puerto Rico (Velez-Juarbe & Domning, 2014) and are about 28 Ma (range 26-30, Ma,

Early to Late Oligocene) (Velez-Juarbe & Wood, 2018). While a few taxa have been proposed as older stem-dugongids, until statistical methods yield a congruent estimate, we advocate a conservative approach that uses *Priscosiren* (or *Caribosiren*) to mark the minimum age of the dugongid lineage.

Stem-Tubulidentata. The fossil taxon *Myorycteropus africanus* from the Napak IV locality in Uganda is the oldest known stem-tubulidentate (Holroyd, 2010b). The age of this site is approximately 19.5 Ma (range 19-20 Ma, Burdigalian, late-Early Miocene).

Stem-Macroselidea. *Chambius kasserinensis*, from the CBI-1 Djebel Chambi locality at the Kasserine Plateau in Tunisia, is the earliest known stem-macroselidean (Tabuce, 2018). Based on shared mammalian and charophyte taxa, CBI-1 has been interpreted as approximately contemporaneous with the mammal bearing sites of the Glib Zegdou Formation in Algeria (Seiffert 2010a). The age of these sites have been correlated with the upper half of magnetochron C21n or the upper half of C22n (Coster et al., 2012). A span of 46.3-49.4 Ma (late Ypresian to early Lutetian) includes the range informed by magnetostratigraphy and a mid-point of 47.85 Ma should be a sufficient point estimate for this calibrating taxon.

Stem-Macroselidea. An additional fossil macroselidean, *Metoldobotes*, can be used as a secure calibrator. The earliest known specimens of this genus are from the L-41 site, Jebel Qatrani Formation, Fayum, Egypt. *Metoldobotes* is younger than *Chambius* and is more closely related to the crown-clade (Cooper et al., 2014). The age of L-41 is about 34.5 Ma (range 33.9-35 Ma, terminal Priabonian, latest-Late Eocene) (Gunnell et al., 2018; Seiffert, 2006).

Stem-Rhynchocyoninae. The genetic distances between the living species of the genus *Rhynchocyon* are notably small (Carlen et al., 2017). This indicates that the common ancestor of extant *Rhynchocyon* lived in the (relatively) recent past – perhaps only about 8 million years ago (Heritage et al., 2020). However, a few fossil taxa that can be clearly identified as rhynchocyonines are present in East Africa during the Early Miocene, some 18-23 million years ago. Given this large temporal gap, we consider it highly likely that the earliest rhynchocyonines are stem-taxa (Holroyd, 2010a; Novacek, 1984). *Miorhynchocyon meswae*, from the Muhoroni Agglomerate at the Meswa Bridge locality in Kenya is the oldest stem-rhynchocyonine from the Miocene. With an approximate age of 22.5 Ma, this taxon has been used as a calibrator in several molecular phylogenies. However, recent paleontological work at the Songwe Member (site TZ-01S) of the Nsungwe Formation in Tanzania has yielded the slightly older stem-rhynchocyonine *Oligorhynchocyon songwensis* (Stevens et al., 2021). This Tanzanian site is well-dated at about 25 Ma (Roberts et al., 2012), and therefore pushes the minimum age for the origin of the subfamily Rhynchocyoninae back to the latest Oligocene.

Stem-Afrosoricida. The oldest fossil specimens of *Todralestes variabilis* are from the Adar Mgorn 1 locality in the Ouarzazate Basin of Morocco. The age of this site is regarded as Upper Thanetian (terminal Paleocene, 56-57.6 Ma) (Augé & Rage, 2006). Some previous cladistic studies (Seiffert, 2010b) agree with our recent Bayesian analyses that the most probable phylogenetic position of *T.*

variabilis is as a basal stem-afrosoricid. A reasonable point estimate for the age of this taxon is 56.8 Ma.

Stem-Chrysochloridea. The Early Oligocene (Rupelian) species *Eochrysochloris tribosphenus* shares apomorphic dental features with extant golden-moles and the Miocene chrysochlorid *Prochrysochloris*. Other *Eochrysochloris* anatomy resembles an ancestral-grade for afrosoricids. Considering morphology and temporal provenance, *Eochrysochloris* has been interpreted as the earliest known stem-chrysochlorid (Asher, 2010; Seiffert et al., 2007). Specimens are from Quarry E, Jebel Qatrani Formation, Fayum, Egypt – which is about 32.1 Ma with

a range of 31–33.2 Ma (Gunnell et al., 2018; Seiffert, 2006).

Earliest-Afrotheria. Three fossil taxa – *Ocepeia daouiensis*, *Abdounodus hamdii*, and *Eritherium azzouzerorum* – are the earliest known afrotheres (Gheerbrant, 2009; Gheerbrant et al., 2016; Gheerbrant et al., 2001). The proposed phylogenetic positions of these species differ among analytical methods and data sets, suggesting that (variably) they could be stem-afrotheres, stem-paenungulates, or primitive affiliates of the paenungulate orders. Nevertheless, all three are from Sidi Chennane, bed

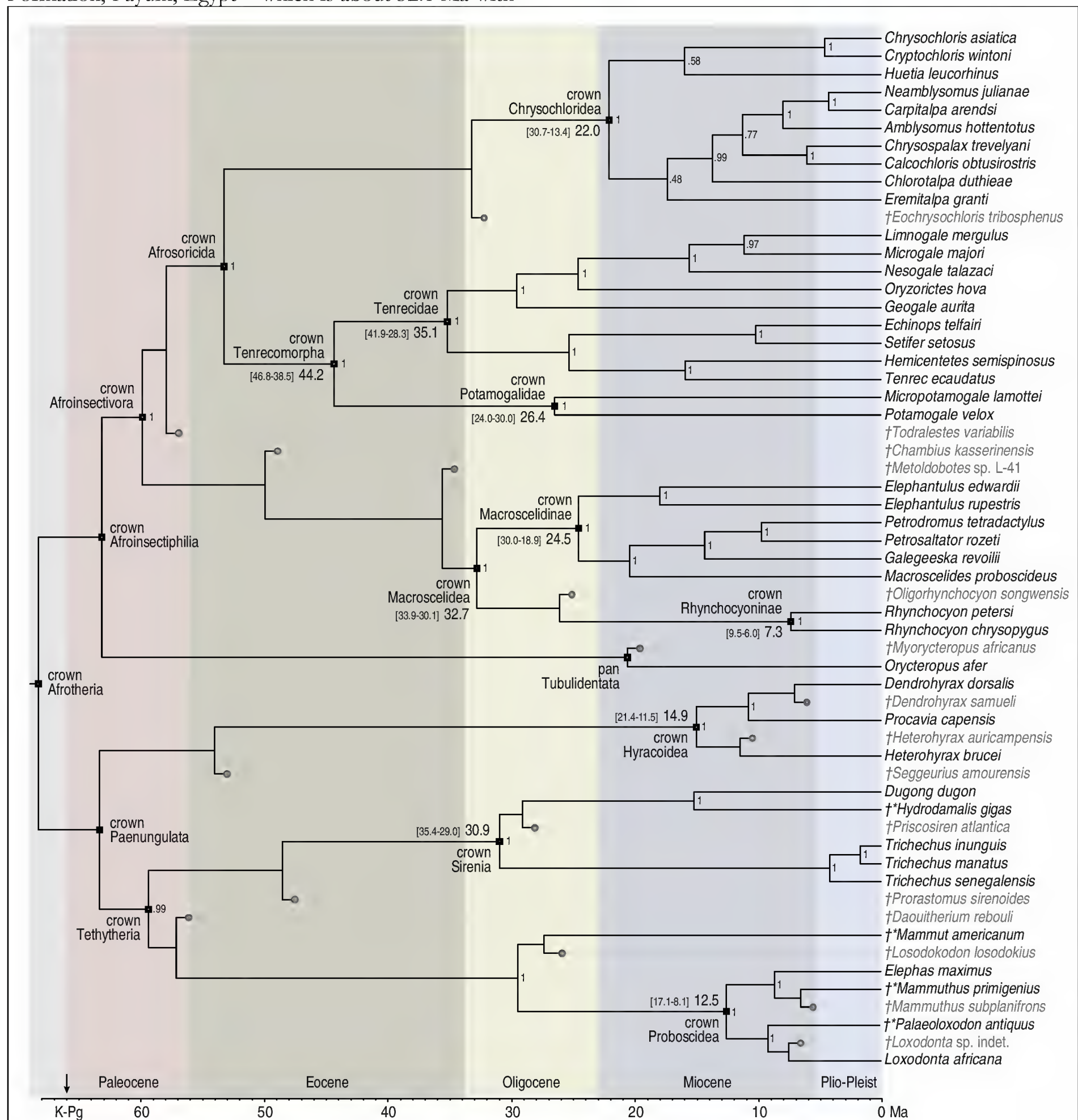


Figure 2. Time-scaled Bayesian phylogenetic estimate for Afrotheria. Daggers indicate extinct taxa, and daggers with asterisks denote recently extinct taxa for which there are genetic data. Units along the x-axis are in millions of years (Ma). Values to the right of nodes are posterior probabilities of splits. Nodes that omit these values were topologically constrained (i.e., to place calibrators, or for tree rooting). For select clades, values to the left of nodes indicate median age estimates with bracketed 95% highest posterior density intervals. Confidence intervals for all other nodes are available in the electronic supplement.

IIa (see stem-Proboscidea above). Phylogenetic estimates consistently place *Eritherium* as nested within crown-Afrotheria so this taxon bears directly on the minimum age of the clade. We advocate an approach that uses 60.5 Ma as a hard minimum for the Afrotherian root node (i.e., the age of bed IIa plus 0.5 million years). Deeper age estimates can be sampled from a truncated normal distribution that is unbounded but softly constrained by the spread parameter.

Other Considerations

There are certainly fossils that have been proposed as the earliest stem (or crown) tenrecomorph, tenrecid, or trichechid taxa. However, despite the relatively secure ages of these candidates, their phylogenetic placements are (in our opinion) not yet well-resolved. For these clades, we have elected to forgo recommendations for fossil calibrators at this time.

The rate at which a gene segment evolves informs the temporal model in a time-scaled analysis. If only one, or few, conservative (i.e., slowly evolving) genes are included in a molecular data set, the nodal age estimates in the resulting tree will almost certainly be impacted. A more balanced approach is to compile multiple gene segments that evolve at different rates. Further, selecting only one fossil taxon to calibrate a time-tree is probably ill advised.

While a molecular study of a single afrotherian order may be improved by the inclusion of several other orders so that external age calibrations can be applied, it is probably extraneous and unnecessary to sample placental mammals outside of the Afrotheria. In practice, this will require a tree rooting strategy that does not select a non-afrothere as the ultimate outgroup taxon. Multiple previous molecular studies of mammalian phylogeny have recovered a strongly supported basal split within Afrotheria with descendant lineages leading to the clades Paenungulata and Afroinsectiphilia. Provided that an afrothere data set samples taxa on both sides of this split, rooting on one of these stem lineages (e.g., the tree edge leading to Paenungulata) should be uncontroversial.

Results & Discussion

The time-scaled analysis presented here differs from comparable studies simply by incorporating calibrating fossils in the data set. At this time, we prefer this approach to “node calibrations” because it yields a tree that is graphically transparent about the age, phylogenetic placements, and number of underlying calibrators. Both strategies effectively enforce a minimum bound for the age of the target node.

Figure 1 plots the ages and localities of key calibration taxa and Figure 2 reports our phylogenetic results. This time-tree is a working hypothesis for the diversification ages among Afrotheria and we acknowledge that future modifications of this data set will shift these age estimates (e.g., by adapting the taxon sample, calibration ages, or genetic loci – or perhaps using a different data set/method altogether). A Bayesian tip-dating analysis of a combined-evidence data set (DNA & morphology, extant & extinct taxa) would further refine these results. Posterior probability support is high for splits throughout most of the tree. However, within the clade Chrysochloridea (where additional genetic sampling is most needed), some support values indicate that proposed relationships should be considered tentative.

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Research Updates

Diamond mine or gold mine? Using eDNA to identify golden moles along the west coast of South Africa

Introduction

Golden moles (Chrysochloridae) represent one of the most threatened mammal groups in southern Africa (IUCN, 2021). The west coast of South Africa is an important but under-surveyed part of their range. Vast stretches of the coastal dune habitats have been severely impacted by alluvial diamond mining over the past century (Fig. 1), and rapidly developing residential areas and agriculture have continued to transform large sections of these habitats, particularly over the past two decades (Fig. 1a,b). This has created concern among conservationists for the conservation status and continued survival of golden mole species in these dune ecosystems. In spite of the prevailing diamond mining activities, we are interested in finding a shimmer of the “living gold” of the Chrysochloridae that potentially still exists here, and when we do, devising plans to protect it.



Figure 1. Mining and residential development on the west coast. Jacobsbay in 2003 (a) and 2021 (b) illustrating the increase in residential development (Source Google Earth). c) Approximate distribution of golden moles along the west coast. d) Habitat destruction resulting from diamond mining in the area north of Port Nolloth. Photos: Samantha Mynhardt.

In 2019 the Endangered Wildlife Trust’s Drylands Conservation Programme (DCP) partnered with the University of Pretoria (UP) to investigate the presence and distribution of two of the most elusive golden moles, namely the Critically Endangered De Winton’s golden mole (*Cryptochloris wintoni*) and the Endangered Van Zyl’s golden mole (*Cryptochloris zyl*) (IUCN, 2021). Golden moles are considered highly elusive due to their behavioural ecology and the fact that they are exclusively subterranean. In the

case of these coastal species, this is exacerbated by the fact that their foraging burrows, otherwise typically visible on the surface of the ground, do not remain visible in sand, especially in the windy coastal conditions characterising the west coast.

Detection and distribution mapping of elusive species is one of the major challenges of biodiversity surveys, which are crucial for the successful implementation of large-scale conservation efforts. For terrestrial mammals in particular, live trapping is still a common detection strategy, but may be invasive, labour-intensive and generally requires onerous permitting. In addition, the type of trap, bait and sampling design can strongly affect the detection probability of particular species (Bovendorp et al., 2017; Harkins et al., 2019). Camera trapping is increasingly used, but this approach is also labour-intensive and costly, and may require long-term coverage and demand substantial maintenance and post-processing (Burton et al., 2015). Camera trapping would also not be ideally suitable for detecting moles “swimming” sub-surface in dunes.

Terrestrial environmental DNA (eDNA) is poised as an effective alternative to existing monitoring approaches (Deiner et al., 2017; Leempoel et al., 2020). For animals, the premise of eDNA is that pieces of skin, hair, faeces or saliva are shed in the environment and that, by collecting environmental samples such as water or soil, we should be able to identify to which species the extracted DNA belongs (Leempoel et al., 2020). eDNA techniques have developed rapidly over the past decade, and particularly in the past three years (Rodríguez-Ezpeleta et al., 2021), and are now increasingly applied to aquatic samples (e.g. Dugal et al., 2021; Port et al., 2016; Ushio et al., 2017), and a handful of primarily proof-of-concept studies exist in which soil samples are used as a source of eDNA (Andersen et al., 2012; Leempoel et al., 2020; Taberlet et al., 2012). Since golden moles are morphologically cryptic, precluding the possibility of visual species identification, eDNA presents an opportunity for simultaneously detecting presence and identifying species.

We hope that by employing eDNA techniques to detect golden moles we could push the envelope on the use of terrestrial eDNA from soil (as opposed to aquatic eDNA) and that finding the golden moles, in particular De Winton’s, would position these species as flagships for a renewed conservation focus on this coastline.

Our ongoing project

We have conducted two independent expeditions to the west coast to collect eDNA samples in the hope of locating and identifying golden moles from this region and learning more about the threats they face. The team consisted of Samantha Mynhardt (UP) and Cobus Theron (DCP), Jean-Pierre le Roux (DCP) and Esther Matthew (DCP), as well as Jessie, our trusted scent-detection dog (Fig. 2).

Our first trip was to Lambertsbay (Fig. 1), which represents the type locality for van Zyl’s golden mole, and one of only two sites at which this species has been recorded (the other site being Groenriviermond, some 150 km further north along the coast; see Fig. 1)(Bronner & Asher, 2016b; Helgen & Wilson, 2001; Taylor et al., 2018). Lambertsbay also overlaps with the currently accepted distribution ranges of the Cape golden mole (*Chrysochloris asiatica*) and Grant’s golden mole (*Eremitalpa granti*)(Taylor et al., 2018). The second trip was aimed at Port Nolloth and the adjacent stretches of coastline that have been impacted

by diamond mining. Port Nolloth represents the type locality for De Winton's golden mole, known from only this locality, and which has not been recorded for more than 80 years (last recorded in the wild in 1937) (Bronner & Asher, 2016a). Although, categorized as Critically Endangered (IUCN, 2021), it is yet to be determined whether this assessment is due to extinction owing to threats posed by mining and habitat destruction, or simply due to the challenges associated with locating and identifying these animals.



Figure 2. The golden mole research team, left to right: Esther Matthew, Cobus Theron holding Jessie, our scent detection dog, Samantha Mynhardt and Jean-Pierre le Roux. The project is funded by Re:wild. Photo: Nicky Souness.

We found surprisingly high levels of golden mole activity in both regions of the west coast, although the effects of habitat transformation on the diamond mine sites were evident, and significantly less activity was found at these mining sites. We collected soil samples for eDNA from golden mole burrows wherever we found signs of recent activity, and also captured one specimen at Lambertsbay, through extensive trapping efforts, for the purpose of matching morphological characteristics to genetics (Fig. 3).



Figure 3. The golden mole specimen captured (and released) at Lambertsbay. Photo: Jean-Pierre le Roux.

Soil eDNA samples were collected by scraping soil from the inner walls of subsurface foraging burrows, wherever these were found to be intact, and from loose soil approximately 2cm below the surface (the depth at which moles typically burrow when foraging), wherever burrow traces were found in soft sand, which collapses as the moles move through it (Fig. 4). The soil samples are now in the laboratory at the University of Pretoria, where we are conducting eDNA extraction, following the methods of Taberlet *et al.* (2012) and Leempoel *et al.* (2020), and have already seen preliminary success in extracting, amplifying and sequencing mammalian eDNA.



Figure 4. Soil eDNA samples were collected by excavating subsurface foraging burrows by slicing neatly through them with a spade and scraping soil from the inner walls, wherever these were found to be intact. Photos: Endangered Wildlife Trust.

We aim to amplify two mitochondrial genes and one nuclear intron in each of the 100+ soil samples collected, using universal mammal primers that will facilitate amplification of all mammalian DNA in the samples, and thus enable identification of other mammalian species in addition to the golden moles. We will send these amplification products (amplicons) for next-generation amplicon sequencing at the Central Analytical Facility (CAF) at Stellenbosch University. This approach involves pooling multiple libraries (samples tagged with unique identifiers) onto a single sequencing chip. Since there is a cost involved in the tagging of libraries, the most cost-effective approach is to pool multiple samples from a single sampling site into a single library. Although this will not complicate species identification, since all unique sequences, and therefore all the mammalian species in the pooled library, will be individually detectable, the drawback to this approach is that we would not be able to pinpoint the exact GPS locations of samples that test positive for presence. However, the way that libraries have been structured will provide us with good insights into which regions require further investigation.



Figure 5. a) Moisture on the surface of the soil greatly enhances detectability of golden mole burrows, which leave a noticeable ridge on the surface. **b)** Surface ridges are less visible in soft dry sand, which collapses as moles move through it, although slightly deeper burrows, such as this one, may still remain intact. Photos: Samantha Mynhardt.

The time we have spent in these dune environments has really revealed to us the harshness of the habitat and the challenges that it holds for golden mole research and conservation. As a team, we found that moisture, either in the form of rain or early-morning dew, played a crucial role in our ability to detect golden mole activity. Moist sand results in higher visibility of subsurface foraging burrows, and also facilitates targeted eDNA collection, since burrows can be excavated and scraped rather than collecting soil from the approximate vicinity of the burrow (Fig. 5).

The fact that very few pristine sites were encountered on either of the expeditions is disconcerting and points to an urgent need to firm up conservation planning and interventions for these species. Furthermore, we found that general public perceptions around golden moles are still highly prejudicial and persecutory; these perceptions often relate to the perceived damage that the sub-surface foraging burrows cause to lawns, particularly on golf courses, and the reaction is typically to seek out means to “eradicate” the animals. These attitudes need to be reversed in order to protect the species better.

Conservation impact

While we await sequencing results, it is clear that the eDNA technique is a potential game changer in the search for cryptic species. The fact that more than 100 good quality samples were collected in less than two weeks is a vast improvement over conventional approaches. The non-invasive nature of the approach is also preferable when working with critically endangered species.

Current land uses and ownership patterns are important considerations that will greatly impact the kind of conservation options that can be considered. We have surveyed across public lands, state land, private land and communal land. The variation in land use and ownership may mean that different models will need to be applied across the west coast.

Options for conservation of habitat would include: declaration of land as contract nature reserve under the provincial biodiversity stewardship process; Conservation Agreements; conservation servitudes; outright purchase or leasing of sites for conservation. In addition, there are also a number of actions we can promote amongst members of the public to ensure better protection of golden moles. These include: keeping domestic dogs leashed on beaches with high mole activity; highlighting the ecological importance of moles in gardens; discouraging the use of poisons in gardens; encouraging the establishment of indigenous gardens; providing more concise inputs in environmental processes concerning coastal developments and mining applications.

Conclusion

As a result of using eDNA, we have developed a highly efficient and effective way of detecting and identifying golden moles and mapping their distribution. This will facilitate planning of conservation action for the ecosystems in this region and for these species. The development of the approach and techniques have also pushed the boundaries of eDNA in applied conservation.

While there is a very good chance that follow-up work will be required for the eDNA study, the progress made in discovering the moles of the west coast is beyond our expectations. Some of our preliminary results already point towards a much more nuanced understanding of the species present on the coast.

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Description of a New Tree Hyrax Species from West Africa

In *Afrotherian Conservation* Number 11, Bearder et al. (2015) hypothesized that an evolutionarily distinct tree hyrax population occurs between the River Niger in Nigeria and the River Volta in Ghana. This conclusion was based on hearing and recording very distinctive nocturnal loud calls produced by hyraxes inhabiting forests in south-western Nigeria, southern Benin, southern Togo and south-eastern Ghana, along with a preliminary examination of the skulls and skins of tree hyraxes in the Natural History Museum in London. These “barking” calls were very different from the typical “klaxon” call of *Dendrohyrax dorsalis* heard to the east and west of this interfluvial region. Based on these observations, we surmised that the Niger-Volta population belonged to a separate species, which we referred to as the “Benin tree hyrax.”

After that article was published, we conducted further field work in the Volta Region of Ghana. We confirmed the observations of Dowsett-Lemaire & Dowsett (2011) that in the Kalakpa Resource Reserve in the Volta Region, the Benin hyrax is sympatric with *D. dorsalis*. We went on to assemble and study a larger library of tree hyrax call recordings from across the Guineo-Congolian forest region, and we recruited experts to undertake detailed morphometric studies of skulls and to analyse DNA from tissue samples. Eric Sargis of Yale University and Neal Woodman of the Smithsonian Institution measured 69 skulls of adult hyraxes in six museum collections in Europe and the USA, while Philippe Gaubert at the University of Toulouse analysed mitochondrial DNA extracted from six tissue samples collected between the Volta and Niger, along with 14 samples of *Dendrohyrax* tissue collected elsewhere in west and central Africa. In 2019-20, with the help of Edward Wiafe (University of Environment & Sustainable Development, Somanya, Ghana), we obtained camera-trap footage of hyraxes near entrances to den sites in rock outcrops on a forested ridge near the east bank of Lake Volta (Fig. 1).



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Figure 1. Camera-trap image of *Dendrohyrax interfluvialis* near the entrance to a den among rocks at Nyagbo Anyigbe, Volta Region, Ghana.

The results of the morphometric and genetic analyses, combined with our examination of a larger sample of loud calls, strongly support the hypothesis that the Benin hyrax justifies recognition as a distinct species. Details of this multifaceted study have now been published in the

Zoological Journal of the Linnean Society, where we name a new species, *Dendrohyrax interfluvialis* (Oates et al., 2021). Compared with *D. dorsalis*, the skull of *D. interfluvialis* is narrower, with a short upper diastema and narrow nasal choanae. Mitogenomic lineages of *D. interfluvialis* are distinct from those of *D. dorsalis* populations, especially in the case of the mitochondrial gene for which we were able to extract and sequence the largest number of examples, cytochrome *c* oxidase 1 (*cox1*). Recordings of the distinctive loud call of *D. interfluvialis* can be listened to, and compared with the calls of other tree hyraxes, at: <https://www.wildsolutions.nl/vocal-profiles/hyrax-vocalizations/dendrohyrax/>.

To our surprise, camera-trapping at Nyagbo Anyigbe in Ghana indicates that the Benin hyraxes at that site are not only using cave dens among rocks (and moving in and out of these dens on the ground), but also appear to be equally active by day and by night (although we have only heard them giving loud calls at night).

The research by our colleagues has uncovered considerable geographic variation in the skulls of Guineo-Congolian tree hyrax populations as a whole, as well as patterns of genetic relatedness inconsistent with current subspecies taxonomy. These findings indicate that the populations commonly grouped together as *Dendrohyrax dorsalis*, with six subspecies (Shultz & Roberts, 2013), require more detailed study, and probably taxonomic revision. Indeed, further careful, comparative studies of hyraxes as a whole are needed, using a range of analytical techniques, including genetics. We predict that such studies would lead to a taxonomic revision of the family Procaviidae.

The recognition of *D. interfluvialis* as a species restricted to the region between the Niger and Volta Rivers adds to a growing body of evidence that this interfluvial region has a distinct fauna of medium-sized forest mammals, including several endemics. The region warrants much greater conservation attention, because its remaining forests are rapidly disappearing and its mammals are heavily hunted for their meat. Hardly any of the few designated conservation areas within the southern, more forested, section of the Niger-Cross interfluvium are currently well protected.

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More Somali Sengis in Djibouti

In September of 2021, a field survey of birds, bats, and terrestrial mammals in the Republic of Djibouti resulted in new observations and photographs of Somali sengis (*Galegeska revoilii*). Compared to the closest sengi occurrence that was previously reported from Djibouti, one of these sightings is nearly 13 km to the east and the others are about 8 km to the south. These new sengi localities are in the Ali Sabieh Region, near the Djalelo Wildlife Protected Area but outside of its boundaries. These areas have been, to my knowledge, mostly unexplored by field biologists. The new occurrence data expands the documented range of *G. revoilii* within Djibouti.

Over a period of three consecutive days, nine individuals were sighted at six locations. On two occasions and at two different sites, pairs of sengis were quietly sheltering together under a short bush. They each emerged several times, roamed nearby, and then returned to their shared shelters. Presumably these were male-female pairs. At other localities, sengis were observed roaming or running. One individual was found dead but intact – this animal has been collected and preserved for future studies. Sightings 3-6 (see Table 1) were within a 0.1 square kilometer area and all nine animals were observed (or found) between 6:30 and 7:00 am.

Table 1. New occurrence data for Somali sengis in Djibouti.

Site	No. sengis	Geocoordinates	Date/Time	No. photos
1	1	11.339225, 42.945944	2021/09/11 6:55am	0
2	2 (1 dead)	11.299381, 42.866964	2021/09/12 6:35am	0
3	2 (paired)	11.287625, 42.848650	2021/09/12 6:55am	3
4	2 (paired)	11.289875, 42.847208	2021/09/13 6:35am	6
5	1	11.290122, 42.846764	2021/09/13 6:50am	0
6	1	11.289939, 42.846514	2021/09/13 6:59am	0



Figure 1. Somali sengi at site 4. This image depicts a relatively hairy tail-tip and a tail length that seems to considerably exceed head-body length. Photo: Houssein Rayaleh.



Figure 2. Somali Sengi at site 3. Note the grey hair on the dorsum of the hands and feet. Photo: Houssein Rayaleh.

Like other Somali sengi sites in Djibouti, the substrates at these new locations are predominantly rocky with scattered low thorny bushes (mainly *Acacia horrida*, *A. tortilis*, & *A. melifera*). Other mammals observed nearby included Salt's dik-diks, gerenuks, Soemmerring's gazelles, Dorcas gazelles, and abundant Speke's pectinators. Based on previous work, gerbils and spiny mice would also be expected to be present, but these nocturnal taxa were not observed. The habitat is essentially pristine and far enough away from Djibouti City that significant human disturbance seems unlikely. While hiking out to these areas, conversations with nearby goat-herders indicated that sengis are seen frequently and that all local people use the common name *wali sandbeer* to refer to sengis.

For the most part, distinguishing the Somali sengi from other sengis that might occur in the Horn of Africa requires close examination of a few key anatomical traits (e.g., relative tail length and size of second upper incisor). However, some of the new photographs (Figures 1 and 2) clearly depict a hairy tail-tip which (given our study of sengis in Djibouti in 2019) almost certainly indicates the species is *G. revoilii*. Also, the dorsum of the hands and feet are grey rather than pure white, a trait that supports this diagnosis. To date, there are no verifiable records of the Somalian rufous sengi in Djibouti, and it has been several decades since that taxon was last documented in the Horn of Africa.

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Afrotheria News

Tenrecs make the front page

The paper written by many members of the tenrec section of the Afrotheria Specialist Group (Stephenson et al., 2021), that summarises the conservation status of tenrecs, made the front page of the journal *Oryx* when it was finally included in an issue in January 2021. The paper was first published online in May 2019, and from the outset the journal was keen to highlight the results of our assessments, as well as showcase on the cover one of the most charismatic afrotheres, the lowland streaked tenrec. The article was also featured twice in the publisher's blog (Stephenson, 2019, 2021).



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Rock hyraxes featured in Animal Social Networks TV series

A new TV series produced by Canadian company Rotating Planet describes the social networks of animals (see <https://www.rotatingplanet.com/rotating-planet-production-news/les-reseaux-sociaux-des-animaux-en-primeur-sur-arte-geie>). The first episode features the rock hyrax, and was filmed at our study site in Ein Gedi, Israel. Our team, led by Prof. Eli Geffen (Tel Aviv University), Prof. Lee Koren, and Dr. Amiyaal Ilany (both at Bar Ilan University), has been monitoring this population since 1999. We mostly focus on vocalization and social behaviour, and also study hormones, sexual selection, and demography (see, e.g., Barocas et al. 2011. *PloS One*, 6: e22375; Ilany et al. 2013. *Animal Behaviour*, 85: 1397-1405).

The episode tells some of the stories that we observed over the years. The series was first aired on ARTE in July 2021. The trailer (which includes the image captured below) is available on YouTube: <https://www.youtube.com/watch?v=yLe0CA9MX9Q>



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Recent Publications

Aardvarks

- Epps, C. W., Weldy, M. J., Crowhurst, R. S., & Spaan, R. S. (2021). Estimating the distribution and habitat suitability for aardvarks (*Orycteropus afer*) in Kruger National Park, South Africa. *African Journal of Ecology*, 59(4), 854-865.
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Golden moles

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